

Using Molecular Marker Technology for Improvement in Sow Reproductive Longevity

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Summary and Implications

The longevity or productive life of sows is one of the important components that contribute to the economic bottom line of swine production. Involuntary sow culling rates caused by locomotion failure, reproductive failure or death have been growing in recent years causing many females to be culled before they reach their most productive parities and before the investment costs of those females have been recovered. In addition to factors such as management, sow condition, health, nutrition, and facilities, there are likely to be genetic components controlling sow longevity that have yet to be fully identified. Research ongoing at Iowa State University, in conjunction with Sygen and PIC, has focused on identifying the genes associated with variation in sow longevity.

Introduction

Sow longevity has different meanings to different people. In the simplest sense, it is how long a sow lives. For some producers, it is defined as how long a sow remains reproductively functional. Since today's commercial pork industry operates on an ever-shrinking financial margin, a sow has to be productive and pay for costs associated with buying her or the costs to produce her. This means that not only does a sow have to be sound, live "long," and remain reproductively functional, but she must also produce a minimum number of pigs born/weaned per litter and her progeny must perform at minimum growth, composition, and quality standards.

Reducing the number of sows being involuntarily removed from the herd due to locomotion failure, reproductive failure, or death would improve sow longevity and allow selective culling of sows to increase rate of genetic progress. Replacement rates, which include both selective and involuntary culling, are inversely related to a herd's average parities per sow. Higher replacement rates driven by involuntary culling reasons infer that producers are required to lower their selection intensity to maintain herd size. PigChamp records averaged from 2001, 2002 and 2003 indicate that the average parity farrowed of sows is 3.42, the average culling rate is 40.9%, the average death rate is 7.46%, and the average replacement rate is 66.46%. Replacement rates of this magnitude can cause a downward

spiral in herd performance in systems with undersized multiplication efforts, since a heavy demand for replacement gilts may result in sub-standard gilts entering the breeding herd, skewing the parity profile, and reducing pigs sold per sow per year. Additionally, high replacement rates cause welfare concerns from the view of both those inside and outside of the swine industry because of the rate at which sows are leaving the farm due to involuntary culling.

Recent statistics show that there are nearly 6 million breeding sows in the United States. Increasing the number of parities each of these sows produces would have large potential to increase the profitability of swine operations. Using standard net present value calculations for a farrow to finish operation such as a purchase price of \$200 per gilt, an average number born alive/litter of 10.2, 8.5 pigs sold per litter, and an average price of 44 \$/CWT for market hogs, an increase in net present value of \$77.38 per sow could be realized if an operation could increase litters per sow from three to four. Therefore, roughly every tenth increase in would result in a benefit of \$0.23 for every pig marketed in a farrow to finish system. For a farrow to wean operation, using the same purchase price and number born alive/litter as above with an average price per head of \$28 for segregated early weaned (SEW) pigs, and marketing 9 pigs per litter, the net present value per sow would increase by \$45.59 if a sow would have four parities instead of three. This would result in an increased profit margin of \$0.13 for every tenth increase in average parity farrowed per sow for every pig marketed in a farrow to wean system. In 2002, there were 38,852,180 pigs sold in the U.S. from farrow to wean operations and 45,959,882 pigs sold from farrow to finish operations. Therefore, for every increase of one tenth (i.e. 0.1 more litters) in average parity farrowed per sow would raise the profit for these two sectors by over \$15,000,000 per year.

Materials and Methods

The use of molecular genetics has resulted in the identification of genes in model organisms that have shown associations with longevity. Results in these model organisms have shown a clear association between a reduction in caloric intake and increasing longevity as well as reducing the susceptibility to disease in the aging process. Research has shown that in *Saccharomyces cerevisiae* and in *Caenorhabditis elegans* a number of homologous genes are shared in the so called "longevity pathways" and that increased longevity is often the result of inactivation of the pathways that promote growth and a reduction in the oxidative damage and other forms of stress. Mutations in the genes affecting the insulin/IGF-1

like pathways have been shown to cause dwarfism as well as extended lifespan. Furthermore, rodent models have shown that genes associated with tolerance to oxidative stress may also have an effect on the longevity of mice.

The hypothesis that guides this comparative genomics research is that the similarity between the functions of certain genes in the various species studied thus far suggests that the same genes may be associated with longevity in the pig. It is possible that trying to increase sow productive life might not be completely correlated with simple lifespan in model organisms. Therefore, other genes more specific to swine may need to be isolated and examined. Our research has primarily been devoted to genes that are involved in reproduction, serve as antioxidants, regulators of food intake, and those that are involved in the insulin pathway.

Preliminary studies have been performed on three distinct resource populations from industry. The first consists of approximately a thousand sows with almost half having less than five parities and the remaining having more than eight parities. The second population consists of over two hundred sires where complete lifetime production records were recorded on their daughters (minimum of ten daughters per sire). The third population consists of roughly eleven hundred maternal line sows where reproductive traits such as total born, number born alive, and number of stillborns were recorded for up to four parities.

For all genes that were selected, primers were designed from human or pig sequences to amplify specific DNA sequences. The resulting product for each gene was then sequenced to identify polymorphisms (differences in nucleotide bases in the DNA sequence) between animals of different breeds or lines. Once a polymorphism was identified, markers specific to each gene were developed and used to genotype the animals for that specific gene. Genotypes from a subset of our resource populations were first obtained to identify if the polymorphism was associated with longevity. For genes showing an association with

longevity, further genotyping was done on all animals in our resource populations. In addition to the gene's association with longevity or reproductive traits, we examined if the longevity marker was associated (either positively or negatively) with production traits such as days to 230 lbs, loin eye area, backfat, and some meat quality traits. This is done to ensure that selection for increased longevity would not have detrimental effects on other traits of economic interest and this could be viewed as a bonus if the gene has positive effects on other important traits.

Results and Discussion

Recently, PIC has been using reproductive longevity markers in its routine breeding program. Research involving more than ten new candidate genes was initiated recently resulting in three genes to date that have been identified with significant effects on longevity. The size and direction of genotypic effects vary among lines and herds. Depending on the data set examined, these effects vary from 0.2 to over 2 parities increase between different homozygotes. As an added bonus, two of these genes have additive effects on other production traits suggesting that if selection for the beneficial form of the gene is made, then the producer can benefit from improvement in multiple traits at once. Realizing that these are preliminary results for these genes, testing on different and larger populations must be done before these can be used for selection in swine production. However, these results combined with earlier results on other reproductive longevity markers, suggest that sow longevity is influenced genetically, thus breeders have the ability to select the beneficial forms of certain genes to improve the ability of sows to live longer. Future research will continue to focus on more candidate genes involved in reproduction, oxidation, food intake, and the insulin pathway. We will also continue validating the effects we have seen in our candidate genes to date in other swine populations to ensure that they are real and have large enough effects to warrant the use of molecular markers.